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FIG. 1-1

1		M--LSII FKEFVKYNRHVIKTMQIRTCHSITQTLPQ--LPCSSRKAHHRHLLPPLNAAVSAAP--FKARKAHS-----MPPEKKEIF MAATPFLAVAGHGVSKPANAKDSYCFKFASSARTVTLPOIHWRCSRSSHSTGTTTMAVPVLKREKQDEEQWGYLAPEKLEVL M--QAHGI-----AIRARGPVAATQAPARR--RQC-----RVSAAGVAP-----AARARVTHS-----MPPEKAEVF ----- M--QVVG-----TVRVSGGAVVAPS--R--RQC-----RVSAAVLTAETATATARRRVTHS-----MPPEKAEVF M-----QIQTCSYIRIQILP--LP-WARRTGRHKMLPPIAAISATPPSLKSPKTHS-----MPPEKIEIF MALKLHHTAFNPSM--AVTSSGLPRSYHL-----RSHRVFMASSITIGITS-KEIPNAKKPHMPPREAHVQKTHS-----MPPQKIEIF MALLNSTITVAMKQNPVAVSFPRITCLGSSFPRLLRVSCVATNPSTSEETDKKFRPIKEVPNQVTHS-----ITQEKLEIF MALKNPVTTFPS-----TRSLNPFSSR-----SPRPFMAASTFNSTKEAEKLKSHGPPKEVHMVQVTHS-----MPPQKLEIF MALRLNPIPT--Q-----TFSLPQMPSL-----RSPRFRMASTL--RSGSKEVENIKKPTTTPREVHVQVTHS-----MPPQKIEIF	78	KSLEGWASEWVLP LLKPVEQCWQPQNFLPDPS--LPHEEFHQVKELRERTKELPDEYFVVLVGMVMTEDALPTYQTMINNLDGVKDDSGT AHLEPWAFAHVLPLLLKPAFAEAWQPSDMLPDPAALGDEGFHDACRELARAASVPDAHLVCLVGNMITEALPTYQSVNPEAVRDLTGA RSLEGWAARSLLPLLLKPVEECWQPADFLPDSS--SEMFGEHVEVRELARAAGLPDEYFVVLVGMVTEALPTYQTMINNLDGVKDDSGT ----- RSLEGWARSLLPLLLKPVEECWQPTDFLPDSS--SEMFGEHQVHELARAAGLPDEYFVVLVGMITEALPTYQTMINNLDGVKDDSGT KSLEWASQSVLP LLKPVEQCWQPQEFVDPSS--LPFGDFTDQVKALRDRTAELPEEYFVVLVGMITEALPTYQSMINNLDGVKDDSGT KSLEGWAEENVLVHLKPVEKCWQPQDFLPDPA--SEG-FMDQVKELRERTKEIPDEYLVVLVGMITEALPTYQTMNLDGVKDDSGT KSMENWAQENLLSYLKPVEASWQPDFLPETN--DEDRFYEQVKELRDRTKEIPDDYFVVLVGMITEALPTYQTTNLDGVKDDSGT KSLEGWAEENVLVHLKPVEKCWQPQDFLPDPA--SDG-FEEQVKELRERAKELPDDYFVVLVGMITEALPTYQTMNLDGVKDDSGT KSLEDWADQNILTHLKPVEKCWQPQDFLPDPS--SDG-FEEQVKELRERAKEIPDDYFVVLVGMITEALPTYQTMNLDGVKDDSGT	167	SPSPWAVWTRAWTAENRHGDLRLTYLYLSGRVDMKVEKTVHLYISAGMDPGTDNNPILGFVYTSFQERATFVAHGNTARL--AKEGGD DSTAWARWIRGWSAEENRHGDALSHVYMYLSGRVDMRQVDRTVHRHLIASGMAMNAARSPYHGFIYVAFQERATAISHGNMARHVGA--HGD SNCPWAVWTRAWTAENRHGDILGKMYLSGRVDMRMVVEKTVQYLISGMDPGTENNPYLGFIYTSFQERATAVSHGNTARL--ARAGHD -----YLSGRFDMAEVERAVHRLIRSGMAVDPPCSPYHAFVYTAQERATAVSHGNTARLVGARGHGD SACPWAVWTRWTAENRHGDILGKMYLSGRVDMRMVVEKTVQYLISGMDPGTENNPYLGFIYTSFQERATAVSHGNTARL--ARAGHD SPSPWALWTRAWTAENRHGDLRLTYLYLSGRVDMKVEKTVQYLISGMDPGTENNPYLGFIYTSFQERATFVSHGNTARL--AKEGGD SLTSWALWTRAWTAENRHGDLRLNKLYLISGRVDMRQVDRTVHRLIASGMAMNAARSPYHGFIYTSFQERATAVSHGNTARL--AKDHGD SLTPWAVWTRAWTAENRHGDLRLNKLYLISGRVDMRQVDRTVHRLIASGMAMNAARSPYHGFIYTSFQERATAVSHGNTARL--AKDHGD SLTPWALWTRAWTAENRHGDLRLNKLYLISGRVDMRQVDRTVHRLIASGMAMNAARSPYHGFIYTSFQERATAVSHGNTARL--AKDHGD SLTSWALWTRAWTAENRHGDLRLNKLYLISGRVDMKVEKTVQYLISGMDPGTENNPYLGFIYTSFQERATFVSHGNTARL--AKEGGD
SID2 (soy)						
SID10 (corn)						
SID12 (corn)						
SID14 (rice)						
SID16 (rice)						
gi4704824						
gi267036						
gi6957724						
gi3355632						
SID23 (soy)						
SID2 (soy)						
SID10 (corn)						
SID12 (corn)						
SID14 (rice)						
SID16 (rice)						
gi4704824						
gi267036						
gi6957724						
gi3355632						
SID23 (soy)						

FIG. 1-1

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	255		344
SID2 (soy)	PVLARLCGTTAADEKRRHENAYSRIVEKLLLEVDPTGAMVAIGNMMEKKTMPAHLMYDGGDPRLEFEHYSAVAQRIGVYTANDYADILEFLV		
SID10 (corn)	HVLARVCGAIMADEKRRHETAYTRIVAKLFEVDPDAVRAALGYMRHRITMPAALMTDGRDAHLHYAAAAQQTGVYTASDYRSILEHLI		
SID12 (corn)	DVLARACGTTAADEKRRHETAYGRIVEQLQLDPEGAVLAVADMRRKRTMPAHLMDGRDMDLFEHFAAQAQRIGVYTARDYADIVEFLV		
SID14 (rice)	AALARVCGTTAADEKRRHEAAYTRIVSRLLLEADPDAGRAVARMLRRGVAMPTSPISDGRRDDLYACVVSAAEQAGTIVSDYCSIVEHLV		
SID16 (rice)	DVLARTCGTTAADEKRRHETAYGRIVEQLRLDPOGAMLAIAADMHRKRTMPAHLMDGRDMDLFDHFAAQAQRILNVYTARDYADIVEFLV		
gi4704824	PVLARICGTTAADEKRRHENAYSRIVEKLLLELDPTGAMVAIGDMMQKKTMPAHLMYDGEDPKLFDHFSAVAQRMGVYTANDYADILEFLI		
gi267036	FQLAQVCGIITAADEKRRHETAYTKIVEKLFEIDPDGAVLALADMRRKVTMPAHLMDGDKDNLFDHYSAVAQQIGVYTAKDYADILEHLV		
gi6957724	TTLAKICGTTAADEKRRHETAYTRIVEKLFEIDPDGTVQALASMMRRKRTMPAHLMDGRDDDLFDHYAAVAQRIGVYTATDYAGILEFLI		
gi3355632	MKLAQICGIIAADEKRRHETAYTKIVEKLFEIDPDGTVLALADMRRKKTSMPAHLMYDGEDDNLFDNYSVAQRIGVYTAKDYADILEFLV		
SID23 (soy)	IKLAQICGMTIASDEKRRHETAYTKIVEKLFEVDPTGTVMAFADMMRRKKIAMPAHLMYDGRDDNLFDNYSAVAQRIGVYTAKDYADILEFLV		
	345	405	
SID2 (soy)	ERWRLEKLE-GLMAEGKRAQDFVCGIAPRIRLQERADERARKMKHHG-VKFSWIFNKE---LLL	(405 aa)	
SID10 (corn)	RQWRVEELAAGLSGEGRRARDYVCGLPHKIRRMEEKAHDRAAQTQKKPTSVPFWSWIFDRSVNVVIP	(424 aa)	
SID12 (corn)	KRWKLETLESGLSGEGRRARDFVCGIAPRMRRAEAEADRAKK-DEPRM-VKFSWIFDRE---AVV	(380 aa)	
SID14 (rice)	REWRVEELAAGLSGEGRRARDYVCELPPQKIRRMKEKAHERAVKAQKKPISIPINWIFDRHVSVMPLP	(219 aa)	
SID16 (rice)	KRWKLETLETLGSGEGRRARDYVCGIAPRIRLQERADERARKM-DEQRK-VKFSWIYDRE---VIV	(381 aa)	
gi4704824	GRWRLEKVQ-DLKDEGKKAQDFVCGIAPRIRLQERADERARKM-PHA-VKFSWIFNKE---IIL	(384 aa)	
gi267036	NRWKVENL-MGLSGEGHKAQDFVCGIAPRIRLGERAQSLSKPSV-L---VPFSWIFNKE---LKV	(398 aa)	
gi6957724	RRWEVEKLGMLSGEGRRARQDYLCPLPQIRIRLERANDRVKLASKPSVSWIYGRE---VEL	(411 aa)	
gi3355632	GRWKVDAF-TGLSGEGNKAQDFVCGIAPRIRLQERADERARKM-TSKS---VPFSWIFSRE---LVL	(396 aa)	
SID23 (soy)	GRWKVEQL-TGLSGEGRKAQDYVCGIAPRIRLQERADERARKM-T---LKFSWIHDRE---VLL	(391 aa)	

FIG. 1-2